

Replacement Sheet

Figure 1A

Identity to SeqID No:1 is indicated by a dot, and a dash ("—") indicates a missing nucleotide.

	*	20	*	40	*	
Seqid1 :	ATGAATA	CCAAACTGACAAAAA	TCTTTCCGGTCTCTTGTCGCAACCGC	:	50	
Seqid3 :	:	50	
Seqid5 :	:	50	

	60	*	80	*	100	
Seqid1 :	CGCCTTCAGACAGCATCTGCAGGAA	ACATTACAGACATCAAAGTTCC	T	:	100	
Seqid3 :	:	100	
Seqid5 :	G.....	:	100	

	*	120	*	140	*	
Seqid1 :	CCCTGCCCAACAAACAGAAA	ATCGTCAAAGTCAGCTTGACA	AAAGAGATT	:	150	
Seqid3 :	:	150	
Seqid5 :	:	150	

	160	*	180	*	200	
Seqid1 :	GTCAACCCGACC	GGCTTCGTAACCTCCTCACCGGCCGC	ATCGCCTTGGA	:	200	
Seqid3 :	:	200	
Seqid5 :	:	200	

	*	220	*	240	*	
Seqid1 :	CTTGAA	CACAAACCGGCATTTCCATGGAT	CAACAGGTACTCGAATATGCCG	:	250	
Seqid3 :	:	250	
Seqid5 :	:	250	

	260	*	280	*	300	
Seqid1 :	ATCCTCTGTTGAGCAA	AATCAGTGCCGCACAAA	ACAGCAGCCGTGCGCGT	:	300	
Seqid3 :	:	300	
Seqid5 :	:	300	



Replacement Sheet

Figure 1B

*	320	*	340	*
Seqid1 :	CTGGTTCTGAATCTGAACAAACCGGGCCAATACAATACCGAAGTACGCGG	:	350	
Seqid3 :	:	350	
Seqid5 :	:	350	

360	*	380	*	400
Seqid1 :	GAACAAAGTTGGATATTCACTAACGAATCGGACGATACCGTGTCCGCC	:	400	
Seqid3 :	:	400	
Seqid5 :	:	400	

*	420	*	440	*
Seqid1 :	CCGCACGCCCGCCGTAAAAGCCGCCTGCCGCACCGGCAAAACAACAG	:	450	
Seqid3 :	:	450	
Seqid5 :	:	450	

460	*	480	*	500
Seqid1 :	GGCTGCCGCACCGTCTACCAAGTCCGCAGTATCCGTATCAAACCCTTA	:	500	
Seqid3 :	:	499	
Seqid5 :G.....	:	499	

*	520	*	540	*
Seqid1 :	CCCCGGCAAAACAACAG-CTGCCGCACCGTTACCGAGTCCGTAGTATCC	:	549	
Seqid3 :G.....	:	549	
Seqid5 :G.....	:	549	

560	*	580	*	600
Seqid1 :	GTATCCGCACCGTTCAGCCC GGCAAAACAACAGAGCGGGCATCAGCAA	:	599	
Seqid3 :	:	599	
Seqid5 :	:	599	

*	620	*	640	*
Seqid1 :	ACAAACAGACGGCAGCACCAAGCAAAACAACAGACAGGGCAGCACCAGCAAAAC	:	649	
Seqid3 :	:	649	

Replacement Sheet

Figure 1C

Seqid5 :G.....G..... : 649

660 * 680 * 700

Seqid1 : AACAGGCAGCACCAACAGAAAACAAATATCGATTCCGCAAAGAC : 699

Seqid3 : : 699

Seqid5 : : 699

* 720 * 740 *

Seqid1 : GGCAAAATGCCGGCATTATCGAATTGGCTGCATTGGCTTGCCGGCA : 749

Seqid3 : : 749

Seqid5 : : 749

760 * 780 * 800

Seqid1 : GCCCGACATCAGCCAACAGCACGACCACATCGTTACGCTGAAAAACC : 799

Seqid3 : : 799

Seqid5 : : 799

* 820 * 840 *

Seqid1 : ATACCCTGCCGACCACGCTCCAACGCAGTTGGATGTGGCAGACTTAAA : 849

Seqid3 : : 849

Seqid5 : : 849

860 * 880 * 900

Seqid1 : ACACCGGTTCAAAAGGTTACGCTGAAACGCCTCAATAACGACACCCAGCT : 899

Seqid3 : : 899

Seqid5 : : 899

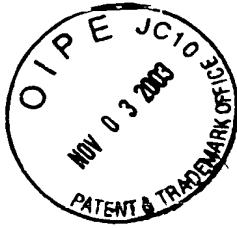
* 920 * 940 *

Seqid1 : GATTATCACAAACAGCCGGCAACTGGGAACTCGTCAACAAATCCGCCGCGC : 949

Seqid3 : : 949

Seqid5 : : 949





Replacement Sheet

Figure 1D

960

*

980

*

1000

Seqid1 : CGGGATACTTACCTCCAAGTCCTGCCGAAAAAACAAAACCTCGAGTCA : 999

Seqid3 : : 999

Seqid5 : : 999

*

1020

*

1040

*

Seqid1 : GGC GGCGTGAACAATGCGCCAAAACCTTCACAGGCCGGAAAATCTCCCT : 1049

Seqid3 : : 1049

Seqid5 : : 1049

1060

*

1080

*

1100

Seqid1 : TGACTTCCAAGATGTCGAAATCCG CACC AT CCTGCAGATTGGCAAAG : 1099

Seqid3 : : 1099

Seqid5 : : 1099

*

1120

*

1140

*

Seqid1 : AATCCGGGATGAACATTGTTGCCAGCGACTCCGTCAACGGCAAATGACC : 1149

Seqid3 : : 1149

Seqid5 :A..... : 1149

1160

*

1180

*

1200

Seqid1 : CTCTCCCTCAAAGACGTACCTTGGGATCAGGCTTGGATTGGTTATGCA : 1199

Seqid3 : : 1199

Seqid5 :G..T..G..... : 1199

*

1220

*

1240

*

Seqid1 : GGCACGCAACCTCGATATGCGCCAACAAGGGAACATCGTCAACATCGCGC : 1249

Seqid3 : : 1249

Seqid5 : ...G.....G.....T..... : 1249

1260

*

1280

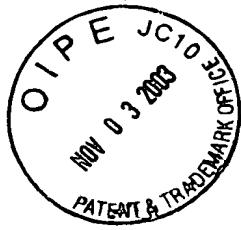
*

1300

Seqid1 : CCCCGGACGAGCTGCTTGCCAAAGACAAAGCCTTCTACAGGCCGGAAAAA : 1299

Seqid3 : : 1299

Seqid5 :C.....A..... : 1299



Replacement Sheet

Figure 1E

* 1320

* 1340

*

Seqid1 : GACATTGCCGATCTAGGCCGCGCTGTATTCACAAAACCTCCAATTGAAATA : 1349

Seqid3 : : 1349

Seqid5 :T.G..T.....C.....G..... : 1349

1360

* 1380

* 1400

Seqid1 : CAAAAATGTGGAAGAACCGCAGCATCCTGCCTGGACAATGCCGACA : 1399

Seqid3 : : 1399

Seqid5 : : 1399

* 1420

* 1440

*

Seqid1 : CAACCGAAACCGCAATACGCTTGTAGCGGCAGGGCAGCGTGCTGATC : 1449

Seqid3 : : 1449

Seqid5 : .G.....C.....A..... : 1449

1460

* 1480

* 1500

Seqid1 : GATCCGCCACCAATACCCTGATTGTTACCGATAACCGCAGCGTCATCGA : 1499

Seqid3 : : 1499

Seqid5 :C.....C..... : 1499

* 1520

* 1540

*

Seqid1 : AAAATTCCGCAAACGTGATTGACGAATTGGACGTACCCGCGCAACAAGTGA : 1549

Seqid3 : : 1549

Seqid5 : : 1549

1560

* 1580

* 1600

Seqid1 : TGATTGAGGCCGTATCGTCGAAGCGGCAGACGGCTTCGCGCGATTG : 1599

Seqid3 : : 1599

Seqid5 : : 1599

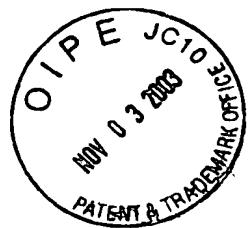
* 1620

* 1640

*

Seqid1 : GGCGTTAAATTGGCGCGACAGGCAAGAAAAAGCTGAAAAATGATACAAG : 1649

Seqid3 : : 1649



Replacement Sheet

Figure 1F

Seqid5 : : 1649

1660 * 1680 * 1700

Seqid1 : CGCATTGGCTGGGGGTAAACTCCGGCTTCGGCGGCGACGATAATGGG : 1699

Seqid3 : : 1699

Seqid5 : : 1699

* 1720 * 1740 *

Seqid1 : GGGCGAACCAAAATCACCTGCCGATTACCGCTGCCGCAAACAGCATT : 1749

Seqid3 : : 1749

Seqid5 : : 1749

1760 * 1780 * 1800

Seqid1 : TCGCTGGTGC CGCGATTCCCTCCGGTGCCTTGAATTGGAATTGTCCGC : 1799

Seqid3 : : 1799

Seqid5 : : 1799

* 1820 * 1840 *

Seqid1 : ATCCGAATCGCTTCAAAAACCAAAACGCTTGCCAATCCGCGGTGCTGA : 1849

Seqid3 : : 1849

Seqid5 : : 1849

1860 * 1880 * 1900

Seqid1 : CCCAAAACCGCAAAGAGGCCAAAATCGAATCCGGTTACGAAATTCTTTC : 1899

Seqid3 : : 1899

Seqid5 : : 1899

* 1920 * 1940 *

Seqid1 : ACCGTAACCTCAATCGCGAACGGCGGCAGCAGCACGAACACGGAACCAA : 1949

Seqid3 : : 1949

Seqid5 : : 1949



Replacement Sheet

Figure 1G

1960

* 1980

* 2000

Seqid1 : AAAAGCCGTCTGGGGCTGACCGTTACGCCAACATCACGCCGACGGCC : 1999

Seqid3 : : 1999

Seqid5 : : 1999

* 2020

* 2040

*

Seqid1 : AAATCATTATGACCGTAAAATCAACAAGGACTCGCCTGCGCAATGTGCC : 2049

Seqid3 : : 2049

Seqid5 : : 2049

2060

* 2080

* 2100

Seqid1 : TCCGTAATCAGACGATCCTGTGTATTCGACCAAAACCTGAATACGCA : 2099

Seqid3 : : 2099

Seqid5 : : 2099

* 2120

* 2140

*

Seqid1 : GGCTATGGTTGAAAACGGCGGCACATTGATTGTCGGCGGTATTTATGAAG : 2149

Seqid3 : : 2149

Seqid5 : : 2149

2160

* 2180

* 2200

Seqid1 : AAGACAACGGCAATAACGCTGACCAAAGTCCCCCTGTTGGCGACATCCCC : 2199

Seqid3 : : 2199

Seqid5 : : 2199

* 2220

* 2240

*

Seqid1 : GTTATCGGCAACCTTTAAAACACGCAGGGAAAAAAACCGACCGCCCGA : 2249

Seqid3 : : 2249

Seqid5 : : 2249

2260

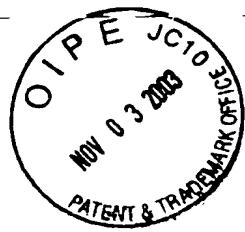
* 2280

* 2300

Seqid1 : ACTGCTGATTTCATACCCCGAGGATTATGGGTACGGCCGGAACAGCC : 2299

Seqid3 : : 2299

Seqid5 : : 2299



Replacement Sheet

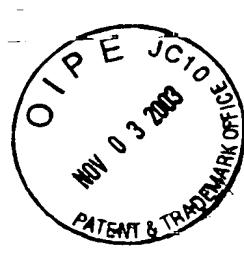
Figure 1H

*

Seqid1 : TGCCTATTGA : 2310

Seqid3 : : 2310

Seqid5 : : 2310



Replacement Sheet

Figure 2A

Identity to SeqID No:2 is indicated by a dot.

* 20 * 40 *
Seqid2 : MNTKLTKIISGLFVATAAFQTA SAGNITDIKVSSL PKQKIVKVSFDKEI : 50
Seqid4 : : 50
Seqid6 : : 50

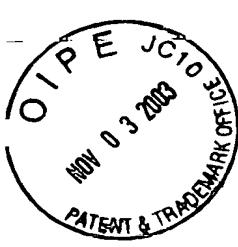
60 * 80 * 100
Seqid2 : VNPTGFVTSSPARIALDFEQTG ISMDQQVLEYADPLLSKISAAQNSSRAR : 100
Seqid4 : : 100
Seqid6 : : 100

* 120 * 140 *
Seqid2 : LVLNLNKGQYNT EVRGNKVWIFINESDDTVSAPARPAVKAAPAAPAKQQ : 150
Seqid4 : : 150
Seqid6 : : 150

160 * 180 * 200
Seqid2 : GCRTVYQVRSIRIQTLYPGKTTAAAPFTESVVSVSAPFSPA KQQAAASAK : 200
Seqid4 : AAAPSTKSAVS VSKPFT.A.QQ..... : 200
Seqid6 : AAAPSTKSAVS VSEPFT.A.QQ..... : 200

* 220 * 240 *
Seqid2 : QQTAAPAKQQTAAPAKQQAAAPAKQTNIDFRKDGNAGIIELAALGFAGQ : 250
Seqid4 : : 250
Seqid6 : ..A.....A..... : 250

260 * 280 * 300
Seqid2 : PDISQQHDHII VTLKNHTLPTTLQRSLDVADF KTPVQKVTLKRLNNNDTQL : 300
Seqid4 : : 300
Seqid6 : : 300



Replacement Sheet

Figure 2B

* 320 * 340 *

Seqid2 : IITTAGNWELVNKSAAPGYFTFQVLPKQNLESGGVNNAPKTFTGRKISL : 350

Seqid4 : : 350

Seqid6 : : 350

360 * 380 * 400

Seqid2 : DFQDVEIRTIQLQILAKESGMNIVASDSVNGKMTLSLKDVPWDQALDLVMQ : 400

Seqid4 : : 400

Seqid6 : : 400

* 420 * 440 *

Seqid2 : ARNLDMRQQGNIVNIAPRDELLAKDKAFLQAEKDIADLGALYSQNFQLKY : 450

Seqid4 : : 450

Seqid6 : L : 450

460 * 480 * 500

Seqid2 : KNVEEFRSILRLDNADTTGNRNTLVSGRGSVLIDPATNTLIVTDTRSVIE : 500

Seqid4 : : 500

Seqid6 : I : 500

* 520 * 540 *

Seqid2 : KFRKLIDELVPAQQVMIEARIVEAADGFSRDLGVKFGATGKKKLKNNTS : 550

Seqid4 : : 550

Seqid6 : : 550

560 * 580 * 600

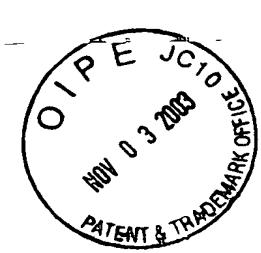
Seqid2 : AFGWGVNSGFGGDDKWGAETKINLPITAAANSISLVRRAISSGALNELSA : 600

Seqid4 : : 600

Seqid6 : : 600

* 620 * 640 *

Seqid2 : SESLSKTCTLANPRVLTQNRKEAKIESGYEIPFTVTSIANGGSSTNTELK : 650



Replacement Sheet

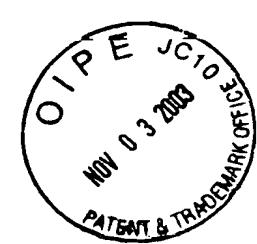
Figure 2C

Seqid4 : : 650
Seqid6 : : 650

660 * 680 * 700
Seqid2 : KAVLGLTVTPNITPDGQIIMTVKINKDSPAQCASGNQTILCISTKNLNTQ : 700
Seqid4 : : 700
Seqid6 : : 700

* 720 * 740 *
Seqid2 : AMVENGGTLIVGGIYEEDNGNTLKVPLLGDIPVIGNLFKTRGKKTDRRE : 750
Seqid4 : : 750
Seqid6 : : 750

760
Seqid2 : LLIFITPRIMGTAGNSLRY : 769
Seqid4 : : 769
Seqid6 : : 769

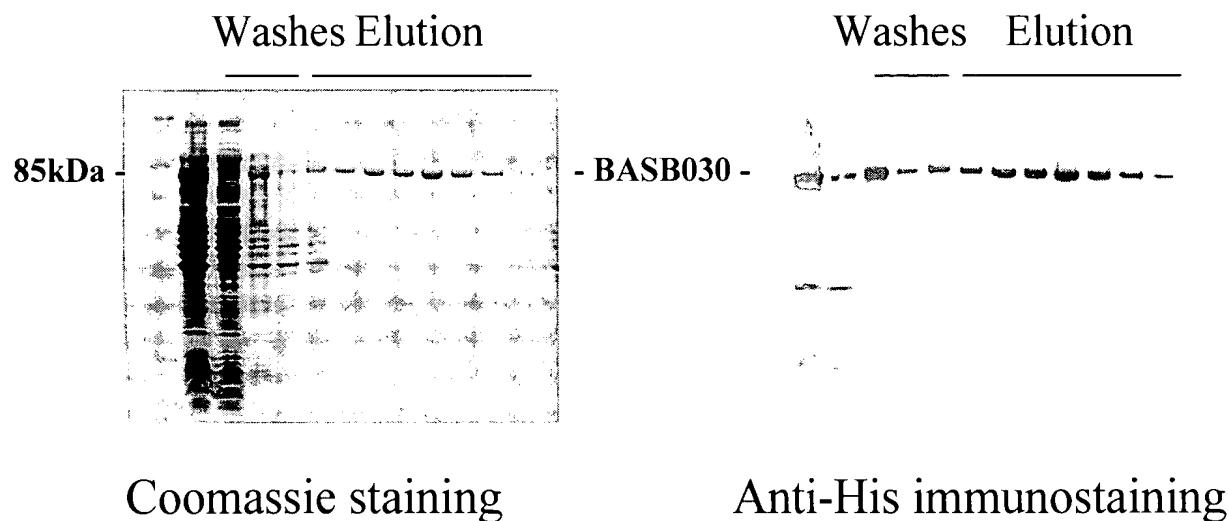


Replacement Sheet

Figure 3

Expression and purification of recombinant BASB030 in *E. coli*.

Substantially pure (more than 80%) BASB030 protein fractions were obtained on a 4-20% gradient polyacrylamide gel (NOVEX) under SDS-PAGE conditions in parallel to a protein molecular weight marker. Gels were either stained with Coomassie Blue R250 or analyzed by western blot using an anti-(His5) monoclonal antibody.

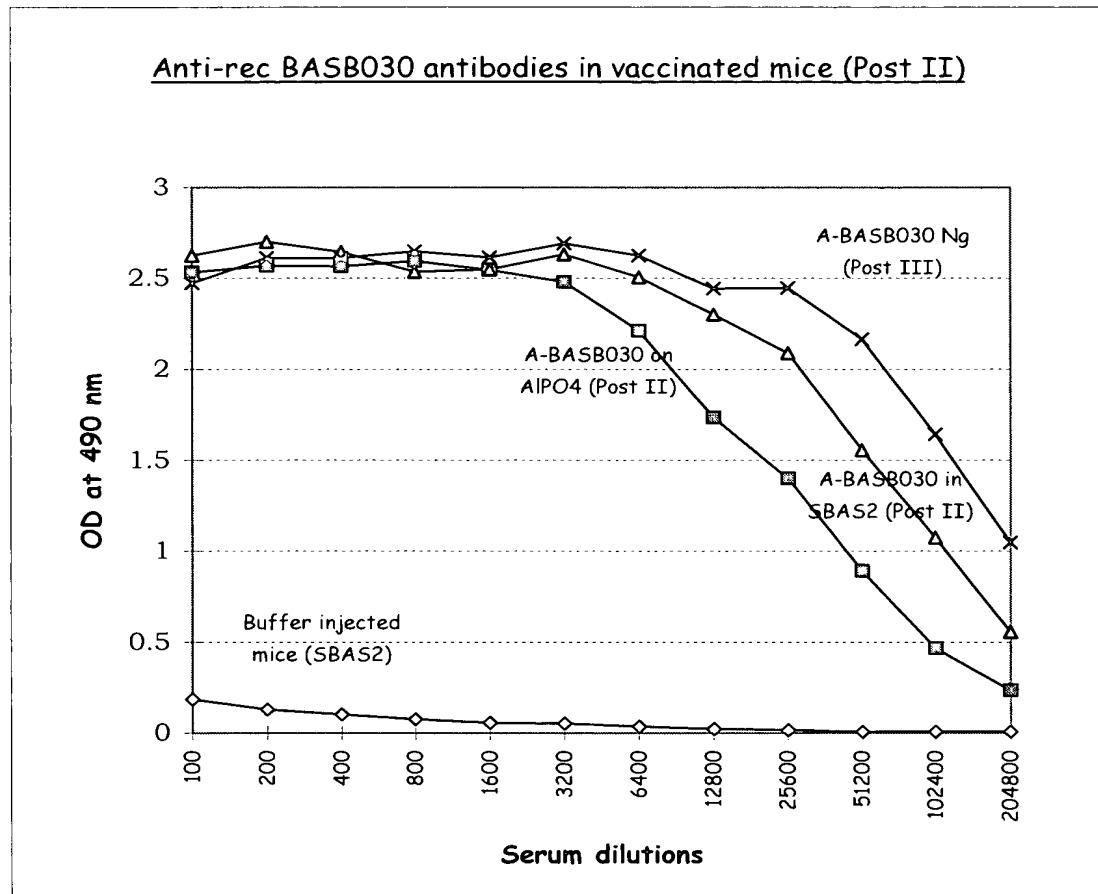


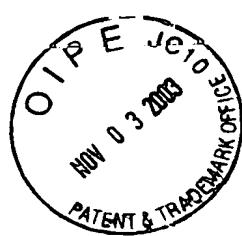


Replacement Sheet

Figure 4

Immunogenicity of the native BASB030 polypeptide. Analysis of the anti-native BASB030 polypeptide on recombinant BASB030 by Elisa.

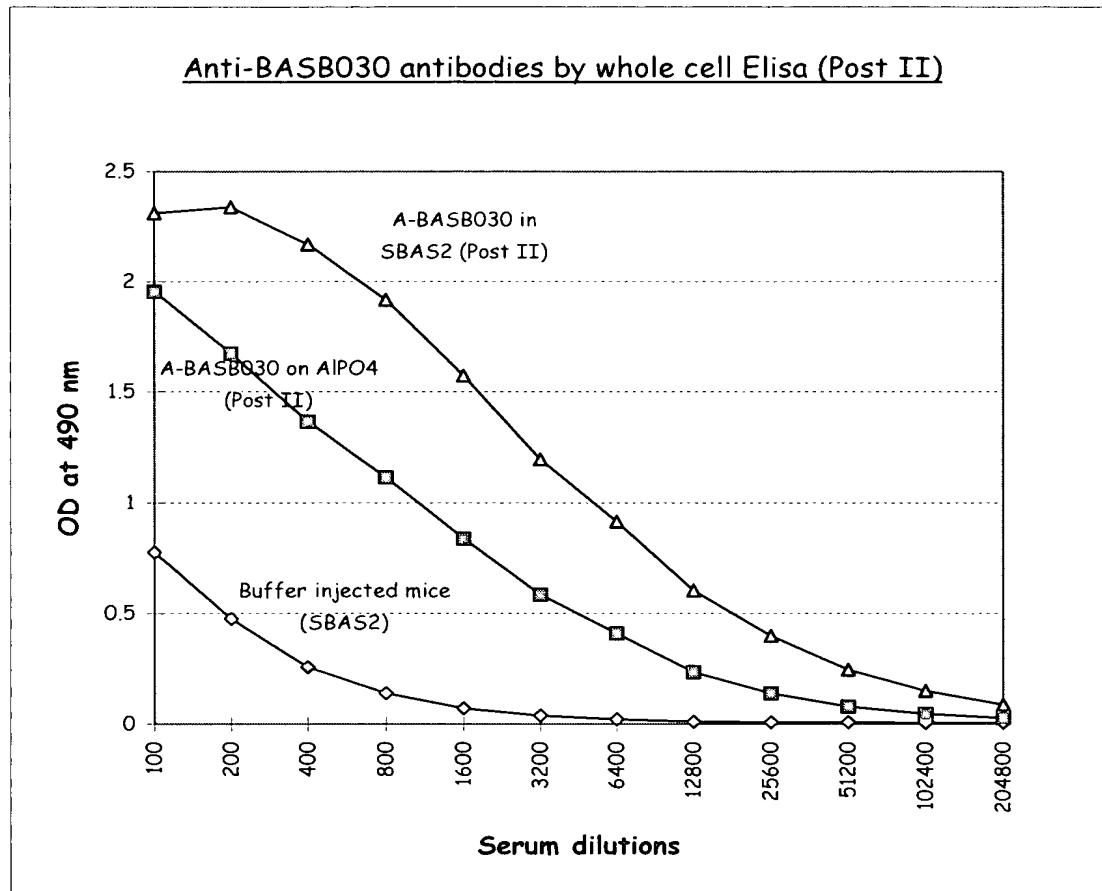


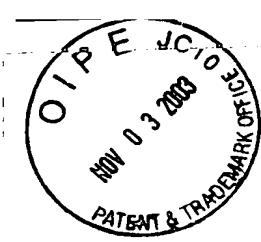


Replacement Sheet

Figure 5

Immunogenicity of the native BASB030 polypeptide. Analysis of the anti-native BASB030 polypeptide response on whole cells by Elisa.

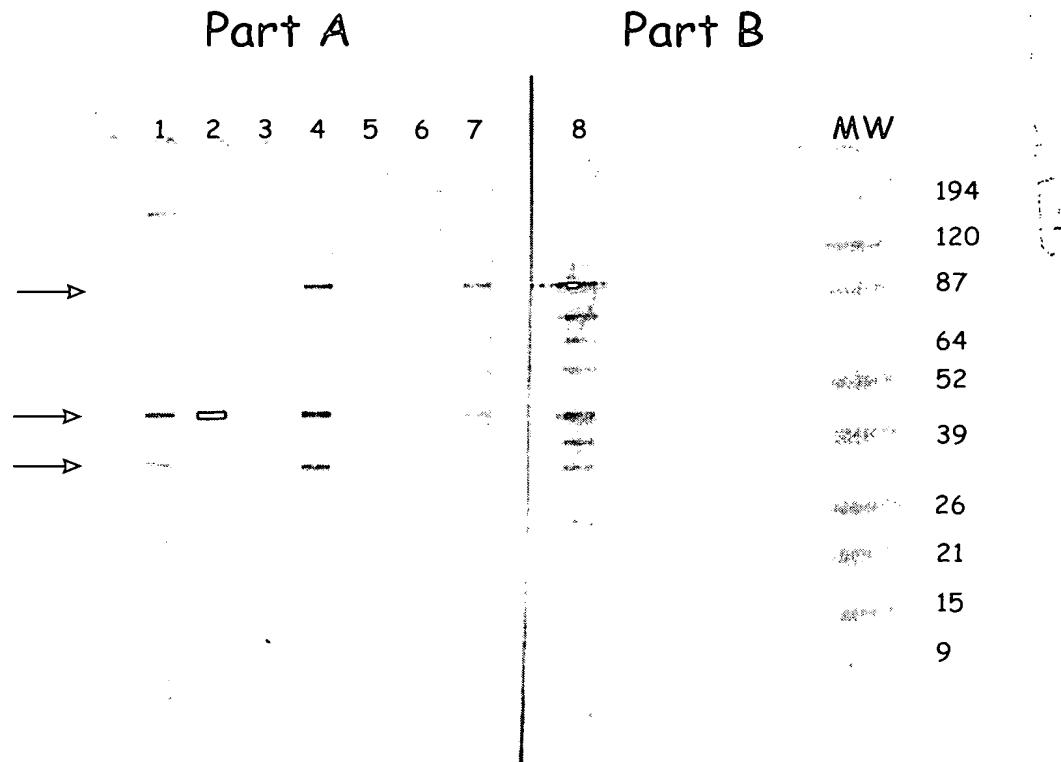




Replacement Sheet

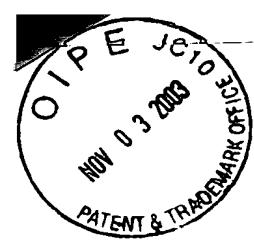
Figure 6

Anti-BASB030 antibodies in human convalescent sera (part A) and in immunized mice (part B) by western-blotting using native BASB030 into the gel.



Lanes :

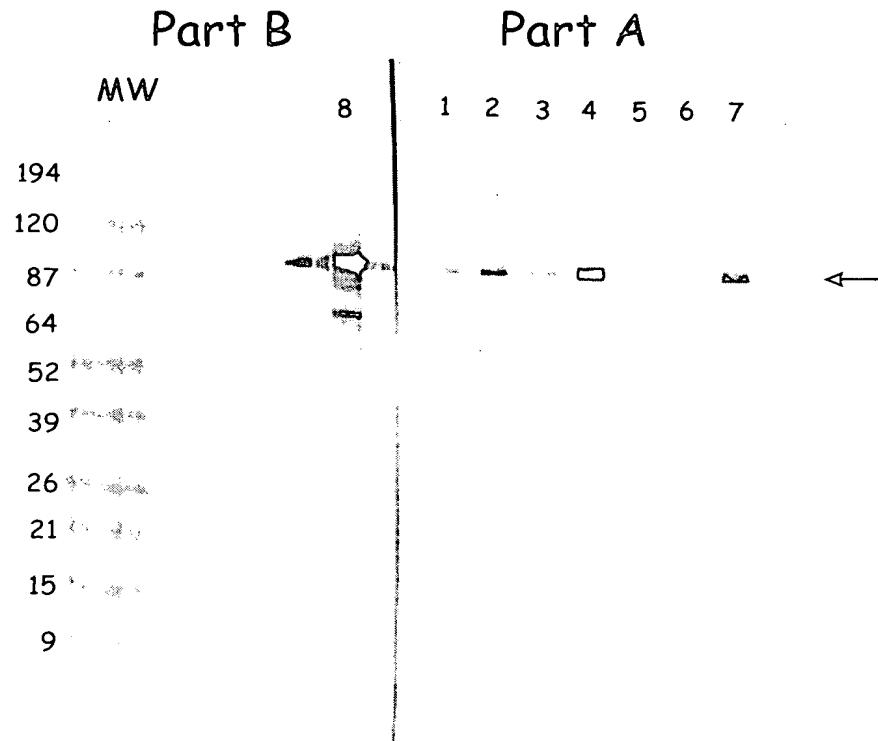
- 1 : convalescent serum n° 262068
- 2 : convalescent serum n° 261732
- 3 : convalescent serum n° 262117
- 4 : convalescent serum n° 261659
- 5 : convalescent serum n° 261469
- 6 : convalescent serum n° 261979
- 7 : convalescent serum n° 261324
- 8 : pool of mice sera imunized with the homolog BASB030 protein from Neisseria gonorrhoeae.



Replacement Sheet

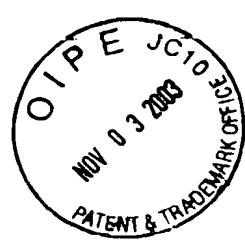
Figure 7

Anti-BASB030 antibodies in human convalescent sera (part A) and in immunized mice (part B) by western-blotting using recombinant BASB030 protein into the gel.



Lanes :

- 1 : convalescent serum n° 262068
- 2 : convalescent serum n° 261732
- 3 : convalescent serum n° 262117
- 4 : convalescent serum n° 261659
- 5 : convalescent serum n° 261469
- 6 : convalescent serum n° 261979
- 7 : convalescent serum n° 261324
- 8 : pool of mice sera imunized with the homolog BASB030 protein from Neisseria gonorrhoeae.



Replacement Sheet

Figure 8

Protective effect of the anti-BASB030 antibodies in the passive protection model

